



PCT09

RAW SEQUENCE LISTING

DATE: 11/13/2003

PATENT APPLICATION: US/09/869,079A

TIME: 17:18:27

Input Set : N:\AMC\US09869079A.raw

Output Set: N:\CRF4\11132003\I869079A.raw

1 <110> APPLICANT: Masure, Stefan
 2 Richardson, Alan
 3 <120> TITLE OF INVENTION: Human AKT-3
 4 <130> FILE REFERENCE: 51869/001
 C--> 5 <140> CURRENT APPLICATION NUMBER: US/09/869,079A
 6 <141> CURRENT FILING DATE: 2002-04-15
 7 <150> PRIOR APPLICATION NUMBER: GB 9828375.7
 8 <151> PRIOR FILING DATE: 1998-12-22
 9 <160> NUMBER OF SEQ ID NOS: 3
 10 <170> SOFTWARE: PatentIn Ver. 2.0
 12 <210> SEQ ID NO: 1
 13 <211> LENGTH: 1547
 14 <212> TYPE: DNA
 15 <213> ORGANISM: Homo sapiens
 16 <400> SEQUENCE: 1

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18   atatataaaa aactggaggc caagatactt ccttttgaag acagatggct cattcatagg 120
19   atataaagag aaacctcaag atgtggattt accttatccc ctcaacaact tttcagtggc 180
20   aaaatgccag ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct 240
21   ccagtggact actgttatag agagaacatt tcatgtagat actccagagg aaagggaaga 300
22   atggacagaa gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat 360
23   gaattgtagt ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac 420
24   aacccatcat aaaagaaaaga caatgaatga ttttgactat ttgaaactac taggtaaagg 480
25   cacttttggg aaagttattt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa 540
26   gattctgaag aaagaagtca ttattgcaaa ggatgaagtg gcacacactc taactgaaag 600
27   cagagtatta aagaacacta gacatccctt tttaacatcc ttgaaatatt ccttcagac 660
28   aaaagaccgt ttgtgttttg tgatggaata tgttaatggg ggcgagctgt ttttccattt 720
29   gtcgagagag cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc 780
30   tgccttggac tatctacatt ccggaagat tgtgtaccgt gatctcaagt tggagaatct 840
31   aatgctggac aaagatggcc acataaaaaat tacagatttt ggactttgca aagaagggat 900
32   cacagatgca gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt 960
33   gttagaagat aatgactatg gccgagcagt agactggtgg ggcctagggg ttgtcatgta 1020
34   tgaaatgatg tgtgggagggt tacctttcta caaccaggac catgagaaac tttttgaatt 1080
35   aatattaatg gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct 1140
36   ttcagggtc ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa 1200
37   agaaattatg agacacagtt tcttctctgg agtaaaactgg caagatgtat atgataaaaa 1260
38   gcttgcacct ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga 1320
39   agaatttaca gctcagacta ttacaataac accacctgaa aaatatgatg aggatggat 1380
40   ggactgcatg gacaatgaga ggcggccgca tttccctcaa ttttcctact ctgcaagtg 1440
41   acgagaataa gtctctttca ttctgtact tcaactgtcat cttcaattta ttactgaaaa 1500
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44 <210> SEQ ID NO: 2
45 <211> LENGTH: 1436

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Re-run is the same as the Entered Copy

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46 <212> TYPE: DNA
47 <213> ORGANISM: Homo sapiens
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51   aaacctcaag atgtggattt accttatccc ctcaacaact tttcagtggc aaaatgccag 180
52   ttaatgaaaa cagaacgacc aaagccaaac acatttataa tcagatgtct ccagtggact 240
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54   gctatccagg ctgtagcaga cagactgcag aggcaagaag aggagagaat gaattgtagt 360
55   ccaacttcac aaattgataa tataggagag gaagagatgg atgcctctac aaccatcat 420
56   aaaagaaaaga caatgaatga ttttgactat ttgaaactac taggtaaaag cacttttggg 480
57   aaagtatttt tggttcgaga gaaggcaagt ggaaaatact atgctatgaa gattctgaag 540
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61   cgggtgttct ctgaggaccg cacacgtttc tatggtgcag aaattgtctc tgccttggac 780
62   tatctacatt ccggaagat tgtgtaccgt gatctcaagt tggagaatct aatgctggac 840
63   aaagatggcc acataaaaat tacagatttt ggactttgca aagaagggat cacagatgca 900
64   gccaccatga agacattctg tggcactcca gaatatctgg caccagaggt gttagaagat 960
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66   tgtgggaggt tacctttcta caaccaggac catgagaaac tttttgaatt aatattaatg 1080
67   gaagacatta aatttcctcg aacactctct tcagatgcaa aatcattgct ttcagggtct 1140
68   ttgataaagg atccaaataa acgccttggg ggaggaccag atgatgcaaa agaaattatg 1200
69   agacacagtt tcttctctgg agtaaactgg caagatgtat atgataaaaa gcttgtacct 1260
70   ccttttaaac ctcaagtaac atctgagaca gatactagat attttgatga agaatttaca 1320
71   gtcagacta ttacaataac accacctgaa aaatatgatg aggatggtat ggactgcatg 1380
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75 <211> LENGTH: 479
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81   Glu Tyr Ile Lys Asn Trp Arg Pro Arg Tyr Phe Leu Leu Lys Thr Asp
82       20           25           30
83   Gly Ser Phe Ile Gly Tyr Lys Glu Lys Pro Gln Asp Val Asp Leu Pro
84       35           40           45
85   Tyr Pro Leu Asn Asn Phe Ser Val Ala Lys Cys Gln Leu Met Lys Thr
86       50           55           60
87   Glu Arg Pro Lys Pro Asn Thr Phe Ile Ile Arg Cys Leu Gln Trp Thr
88       65           70           75           80
89   Thr Val Ile Glu Arg Thr Phe His Val Asp Thr Pro Glu Glu Arg Glu
90       85           90           95
91   Glu Trp Thr Glu Ala Ile Gln Ala Val Ala Asp Arg Leu Gln Arg Gln
92       100          105          110
93   Glu Glu Glu Arg Met Asn Cys Ser Pro Thr Ser Gln Ile Asp Asn Ile
94       115          120          125
95   Gly Glu Glu Glu Met Asp Ala Ser Thr Thr His His Lys Arg Lys Thr

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97	Met Asn Asp Phe Asp Tyr Leu Lys Leu Leu Gly Lys Gly Thr Phe Gly		
98	145	150	155
99	Lys Val Ile Leu Val Arg Glu Lys Ala Ser Gly Lys Tyr Tyr Ala Met		
100	165	170	175
101	Lys Ile Leu Lys Lys Glu Val Ile Ile Ala Lys Asp Glu Val Ala His		
102	180	185	190
103	Thr Leu Thr Glu Ser Arg Val Leu Lys Asn Thr Arg His Pro Phe Leu		
104	195	200	205
105	Thr Ser Leu Lys Tyr Ser Phe Gln Thr Lys Asp Arg Leu Cys Phe Val		
106	210	215	220
107	Met Glu Tyr Val Asn Gly Gly Glu Leu Phe Phe His Leu Ser Arg Glu		
108	225	230	235
109	Arg Val Phe Ser Glu Asp Arg Thr Arg Phe Tyr Gly Ala Glu Ile Val		
110	245	250	255
111	Ser Ala Leu Asp Tyr Leu His Ser Gly Lys Ile Val Tyr Arg Asp Leu		
112	260	265	270
113	Lys Leu Glu Asn Leu Met Leu Asp Lys Asp Gly His Ile Lys Ile Thr		
114	275	280	285
115	Asp Phe Gly Leu Cys Lys Glu Gly Ile Thr Asp Ala Ala Thr Met Lys		
116	290	295	300
117	Thr Phe Cys Gly Thr Pro Glu Tyr Leu Ala Pro Glu Val Leu Glu Asp		
118	305	310	315
119	Asn Asp Tyr Gly Arg Ala Val Asp Trp Trp Gly Leu Gly Val Val Met		
120	325	330	335
121	Tyr Glu Met Met Cys Gly Arg Leu Pro Phe Tyr Asn Gln Asp His Glu		
122	340	345	350
123	Lys Leu Phe Glu Leu Ile Leu Met Glu Asp Ile Lys Phe Pro Arg Thr		
124	355	360	365
125	Leu Ser Ser Asp Ala Lys Ser Leu Leu Ser Gly Leu Leu Ile Lys Asp		
126	370	375	380
127	Pro Asn Lys Arg Leu Gly Gly Gly Pro Asp Asp Ala Lys Glu Ile Met		
128	385	390	395
129	Arg His Ser Phe Phe Ser Gly Val Asn Trp Gln Asp Val Tyr Asp Lys		
130	405	410	415
131	Lys Leu Val Pro Pro Phe Lys Pro Gln Val Thr Ser Glu Thr Asp Thr		
132	420	425	430
133	Arg Tyr Phe Asp Glu Glu Phe Thr Ala Gln Thr Ile Thr Ile Thr Pro		
134	435	440	445
135	Pro Glu Lys Tyr Asp Glu Asp Gly Met Asp Cys Met Asp Asn Glu Arg		
136	450	455	460
137	Arg Pro His Phe Pro Gln Phe Ser Tyr Ser Ala Ser Gly Arg Glu		
138	465	470	475

VERIFICATION SUMMARY

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L:5 M:270 C: Current Application Number differs, Wrong Format